

SEQUENCE LISTING

- <110> Novak, Julia E.
Presnell, Scott R.
Sprecher, Cindy A.
Foster, Donald C.
Holly, Richard D.
Gross, Jane A.
Johnston, Janet V.
Nelson, Andrew J.
Dillon, Stacey R.
Hammond, Angela K.
- <120> NOVEL CYTOKINE ZALPHA11 LIGAND
- <130> 99-16
- <150> US 60/123,547
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- <150> US 60/123,904
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- <150> US 60/142,013
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Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln Asp Arg His	
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Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp Val	
55 60 65	
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Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala Gln	
70 75 80	
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Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile Asn Val Ser	
85 90 95	
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Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala Gly Arg Arg	
100 105 110 115	
cag aaa cac aga cta aca tgc cct tca tgt gat tct tat gag aaa aaa	439
Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr Glu Lys Lys	
120 125 130	
cca ccc aaa gaa ttc cta gaa aga ttc aaa tca ctt ctc caa aag atg	487
Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu Gln Lys Met	
135 140 145	
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Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu Asp Ser	
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 65 70 75 80
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 Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala
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 Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr
 115 120 125
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aargcncary	tnaarwsngc	naayacnggn	aayaaygarm	gnathathaa	ygnwsnath	300
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acntgyccnw	sntgygayws	ntaygaraar	aarccnccna	argarttyyt	ngarmgntty	420
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cac ctt att gac att gtt gaa cag ctg aaa atc tat gaa aat gac ttg His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu 35 40 45	200
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agg agg ctg cct gcc agg agg gga gga aag aaa cag aag cac ata gct Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala 100 105 110	392
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<210> 56

<211> 146

<212> PRT

<213> mus musculus

<400> 56

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Arg His Leu Ile Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp
          35          40          45
Leu Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys
          50          55          60
Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser
65          70          75          80
Asn Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu
          85          90          95
Arg Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile
          100          105          110
Ala Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu
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Leu Ser
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34

<210> 58

<211> 31

<212> DNA

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<223> Oligonucleotide primer ZC22284

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 <223> Oligonucleotide ZC12749

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<210> 60
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<210> 61
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<210> 62
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<223> Oligonucleotide primer ZC22144

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32

<210> 63

<211> 483

<212> DNA

<213> homo sapiens

<400> 63

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atagatatattg ttgatcagct gaaaaattat gtgaatgact tggtcctga atttctgcc	180
gctccagaag atgtagagac aaactgtgag tggtcagctt tttctgttt tcagaaggcc	240
caactaaagt cagcaaatac aggaaacaat gaaaggataa tcaatgtatc aattaaaaag	300
ctgaagagga aaccaccttc cacaatgca gggagaagac agaaacacag actaacatgc	360
ccttcattgtg attcttatga gaaaaacca cccaaagaat tcctagaaag attcaaata	420
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<210> 64

<211> 57

<212> DNA

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<223> Oligonucleotide primer ZC22052

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<210> 65

<211> 57

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<223> Oligonucleotide primer ZC22053

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57

<210> 66
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 <223> Oligonucleotide primer ZC23115

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 <210> 67
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 <400> 67
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 <210> 68
 <211> 35
 <212> DNA
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 <223> Oligonucleotide primer ZC20892

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 <210> 69
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 <400> 69

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<210> 70

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC22054

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<210> 71

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Oligonucleotide primer ZC22055

<400> 71

tgcagtttaa actcaggaat cttcacttcc gt 32

<210> 72

<211> 40

<212> PRT

<213> Artificial Sequence

<220>

<223> Huzalpha11L-1 peptide

<400> 72

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Gln	Leu	Lys	Asn	Tyr	Val	Asn	Asp	Leu	Val	Pro	Glu	Phe	Leu	Pro	Ala
			20					25					30		
Pro	Glu	Asp	Val	Glu	Thr	Asn	Cys								
		35					40								

<210> 73

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> HuzalphallL-3 peptide

<400> 73

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1				5				10					15		
Glu	Arg	Phe	Lys	Ser	Leu	Leu	Gln	Lys	Met	Ile	His	Gln	His	Leu	Ser
			20					25					30		

<210> 74

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23444

<400> 74

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<210> 75

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC23445

<400> 75

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<210> 76

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC447

<400> 76

taacaatttc acacagg

17

<210> 77
 <211> 18
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<220>
 <223> Oligonucleotide primer ZC976

<400> 77
 cgttgtaaaa cgacggcc 18

<210> 78
 <211> 66
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 <223> Oligonucleotide primer ZC22128

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 aatgcg 66

<210> 79
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 <223> Oligonucleotide primer ZC22127

<400> 79
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 gtgttcta 68

<210> 80
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<210> 81
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<210> 82
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<210> 83
<211> 42
<212> DNA
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<400> 83
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<210> 84
<211> 1560
<212> DNA
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<220>

<221> CDS

<222> (1)...(1560)

<223> MBP-human zalphall Ligand fusion polynucleotide

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ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc	96
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr	
20 25 30	
gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc	144
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe	
35 40 45	
cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca	192
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala	
50 55 60	
cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc	240
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile	
65 70 75 80	
acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat	288
Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp	
85 90 95	
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa	336
Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu	
100 105 110	
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa	384
Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys	
115 120 125	
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt	432
Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly	
130 135 140	

aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro 145 150 155 160	480
ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys 165 170 175	528
tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly 180 185 190	576
ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp 195 200 205	624
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325 330 335	
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Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala	
340 345 350	
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Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn	
355 360 365	
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt	1152
Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val	
370 375 380	
ccg cgt gga tcc caa gat cgc cac atg att aga atg cgt caa ctt ata	1200
Pro Arg Gly Ser Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile	
385 390 395 400	
gat att gtt gat cag ctg aaa aat tat gtg aat gac ttg gtc cct gaa	1248
Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu	
405 410 415	
ttt ctg cca gct cca gaa gat gta gag aca aac tgt gag tgg tca gct	1296
Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala	
420 425 430	
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Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn	
435 440 445	
aat gaa agg ata atc aat gta tca att aaa aag ctg aag agg aaa cca	1392
Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro	
450 455 460	
cct tcc aca aat gca ggg aga aga cag aaa cac aga cta aca tgc cct	1440
Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro	
465 470 475 480	

tca tgt gat tct tat gag aaa aaa cca ccc aaa gaa ttc cta gaa aga 1488
 Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
 485 490 495

ttc aaa tca ctt ctc caa aag atg att cat cag cat ctg tcc tct aga 1536
 Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
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<210> 85

<211> 519

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP-human zalpha11 Ligand fusion polypeptide

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 20 25 30
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160

Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
 290 295 300
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val
 370 375 380
 Pro Arg Gly Ser Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile
 385 390 395 400
 Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu
 405 410 415
 Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala
 420 425 430
 Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn
 435 440 445
 Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro
 450 455 460
 Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro
 465 470 475 480
 Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg
 485 490 495

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg
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 Thr His Gly Ser Glu Asp Ser
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 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide primer ZC22849

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 actt 64

<210> 87
 <211> 64
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 87
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<210> 88
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<220>
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<221> CDS
 <222> (1)...(1533)

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cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala 50 55 60	192
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gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu 100 105 110	336
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys 115 120 125	384
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly 130 135 140	432
aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro 145 150 155 160	480
ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys 165 170 175	528

tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly 180 185 190	576
ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp 195 200 205	624
acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala 210 215 220	672
atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys 225 230 235 240	720
gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser 245 250 255	768
aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln 325 330 335	1008

atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala 340 345 350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn 355 360 365	1104
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val 370 375 380	1152
ccg cgt gga tcc cca gat cgc ctc ctg att aga ctt cgt cac ctt att Pro Arg Gly Ser Pro Asp Arg Leu Leu Ile Arg Leu Arg His Leu Ile 385 390 395 400	1200
gac att gtt gaa cag ctg aaa atc tat gaa aat gac ttg gat cct gaa Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu Asp Pro Glu 405 410 415	1248
ctt cta tca gct cca caa gat gta aag ggg cac tgt gag cat gca gct Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu His Ala Ala 420 425 430	1296
ttt gcc tgt ttt cag aag gcc aaa ctc aag cca tca aac cct gga aac Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn Pro Gly Asn 435 440 445	1344
aat aag aca ttc atc att gac ctc gtg gcc cag ctc agg agg agg ctg Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg Arg Arg Leu 450 455 460	1392
cct gcc agg agg gga gga aag aaa cag aag cac ata gct aaa tgc cct Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala Lys Cys Pro 465 470 475 480	1440
tcc tgt gat tcg tat gag aaa agg aca ccc aaa gaa ttc cta gaa aga Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg 485 490 495	1488
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 <212> PRT
 <213> Artificial Sequence

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 <223> MBP-mouse zalphall Ligand fusion polypeptide

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 35 40 45
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
 50 55 60
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile
 65 70 75 80
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp
 85 90 95
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu
 100 105 110
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys
 115 120 125
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly
 130 135 140
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro
 145 150 155 160
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys
 165 170 175
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly
 180 185 190
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp
 195 200 205
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala
 210 215 220
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys
 225 230 235 240
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser
 245 250 255

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro
 260 265 270
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp
 275 280 285
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala
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 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala
 305 310 315 320
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln
 325 330 335
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala
 340 345 350
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn
 355 360 365
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val
 370 375 380
 Pro Arg Gly Ser Pro Asp Arg Leu Leu Ile Arg Leu Arg His Leu Ile
 385 390 395 400
 Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu Asp Pro Glu
 405 410 415
 Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu His Ala Ala
 420 425 430
 Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn Pro Gly Asn
 435 440 445
 Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg Arg Arg Leu
 450 455 460
 Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala Lys Cys Pro
 465 470 475 480
 Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg
 485 490 495
 Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His Leu Ser
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<211> 22

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<223> Oligonucleotide primer ZC22281

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 <223> Oligonucleotide primer ZC22279

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<210> 92
 <211> 31
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 <223> Human zalpha11 Ligand TaqMan probe. ZG32

<400> 92
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<210> 93
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<220>
 <223> Oligonucleotide primer ZC22277

<400> 93
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<210> 94
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gcttgccctt cagcatgtag a

21

<210> 95

<211> 23

<212> DNA

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<220>

<223> Human zalphall1 TaqMan probe. ZG31

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23

<210> 96

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<212> DNA

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<221> CDS

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<223> MBP-zalphall1 soluble receptor polynucleotide
sequence

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48

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr
20 25 30

96

gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe
35 40 45

144

cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala
50 55 60

192

cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile 65 70 75 80	240
acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp 85 90 95	288
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu 100 105 110	336
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys 115 120 125	384
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly 130 135 140	432
aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro 145 150 155 160	480
ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys 165 170 175	528
tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly 180 185 190	576
ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp 195 200 205	624
acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala 210 215 220	672
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gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser 245 250 255	768
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aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln 325 330 335	1008
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala 340 345 350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn 355 360 365	1104
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val 370 375 380	1152
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln 385 390 395 400	1200
acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu 405 410 415	1248

acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc	1296
Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr	
420 425 430	
tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac	1344
Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr	
435 440 445	
acc tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt	1392
Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser	
450 455 460	
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Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser	
465 470 475 480	
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Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr	
485 490 495	
gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa	1536
Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu	
500 505 510	
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515 520 525	
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Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu	
530 535 540	
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Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg	
545 550 555 560	
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Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly	
565 570 575	
tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt	1776
Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe	
580 585 590	

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Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe
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Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala
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His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile
65					70					75					80
Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp
			85					90						95	
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu
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Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys
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Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly
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Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro
145					150					155					160
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys
			165					170					175		
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly
			180					185					190		
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp
		195				200					205				
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala
	210					215					220				

Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys	225			230			235				240
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser		245				250			255		
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro		260				265			270		
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp		275				280			285		
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala		290				295			300		
Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala	305			310			315		320		
Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln			325			330			335		
Met	Ser	Ala	Phe	Trp	Tyr	Ala	Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala			340			345			350		
Ser	Gly	Arg	Gln	Thr	Val	Asp	Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Asn		355				360			365		
Ser	Ser	Ser	His	His	His	His	His	His	Ala	Asn	Ser	Val	Pro	Leu	Val		370				375			380		
Pro	Arg	Gly	Ser	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln	385			390			395		400		
Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu			405			410			415		
Thr	Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr			420			425			430		
Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr		435				440			445		
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Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	465			470			475		480		
Phe	Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr			485			490			495		
Val	Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu			500			505			510		
Asp	Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln		515				520			525		
Tyr	Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu		530				535			540		
Ile	Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	545			550			555		560		

Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly
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580 585 590
Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His
595 600 605

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 <210> 102
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 aaaaaagagt tactcacatt catccatttt acaaagattt ccaggctgca atgggagggc 180
 ttacctctc cctgaaggat gaataaatag gtagcttaac tgacaacctg ttctcagtca 240
 agctgaagtg aaaacgagac caaggctctag ctctactggt ggtacttatg agatccagtc 300
 ctggcaacat ggagaggatt gtcactctgtc tgatgggtcat cttcttgggg acactgggtcc 360
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 ttgttgatca gctgaaaaat tatgtgaatg acttggttaag actatatattg tcacaacaaa 480
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 aagacattag catgattata taggagtata ctgaatttta atgaacttag cggctctaata 720
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 aaaatgctat atttatattc tcataaacta tgtttatctt caagaatctc taagagtact 840
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 <211> 1656
 <212> DNA
 <213> Homo sapiens

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 catctgttaa ctttacaat atatgttgat cattaaactg caagacacta tgcctggcgc 240
 tgtacagaat aaaatgctgc tcaagacatg tcatgataga tacattaaca gaaaccacaa 300
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 acagtgtaa gtttagagcc tcataactca gcaaatgtgt cctaaaccga actaactctc 420

ctttataaaa	cacaaaggtc	ttgtccacca	cccagacatc	aaaatgggtcc	tctgtgtagc	480
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<211> 644

<212> DNA

<213> Homo sapiens

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ataaactaag	aaagcttttt	aaaaatctaa	gtgagcaatc	catatatgaa	aaactgttca	300
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<212> DNA

<213> Homo sapiens

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<210> 109

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC25970

<400> 109

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<210> 110

<211> 36

<212> DNA

<213> Artificial Sequence

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 35 40 45
 Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe
 50 55 60
 Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu
 65 70 75 80
 Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys
 85 90 95
 Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile
 100 105 110
 Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala
 115 120 125
 Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe
 130 135 140
 Cys Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 112
 <211> 153
 <212> PRT
 <213> Homo sapiens

<400> 112
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 Glu Ile Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys
 35 40 45
 Thr Glu Leu Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr
 50 55 60
 Glu Lys Glu Thr Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr
 65 70 75 80

Ser His His Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln
 85 90 95
 Phe His Arg His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg
 100 105 110
 Asn Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala
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 Arg Glu Lys Tyr Ser Lys Cys Ser Ser
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<210> 113
 <211> 162
 <212> PRT
 <213> Homo sapiens

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 Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
 35 40 45
 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
 50 55 60
 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
 65 70 75 80
 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
 85 90 95
 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
 100 105 110
 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
 115 120 125
 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
 130 135 140
 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
 145 150 155 160
 Thr Ser

<210> 114
 <211> 144
 <212> PRT

<213> Homo sapiens

<400> 114

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Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
          35          40          45
Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
          50          55          60
Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65          70          75          80
Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
          85          90          95
Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
          100          105          110
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
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<211> 538

<212> PRT

<213> Homo sapiens

<400> 115

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          20          25          30
Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr
          35          40          45
Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser
          50          55          60
Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr
65          70          75          80
Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val
          85          90          95
Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe
          100          105          110

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	130					135					140				
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225					230					235					240
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Thr	His	Pro	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Val	Pro	Ser
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Pro	Glu	Arg	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	Cys	Ser	Gly	Asp	Phe
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Lys	Lys	Trp	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	Ser	Leu	Glu	Leu	Gly
	290					295					300				
Pro	Trp	Ser	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	Val	Tyr	Ser	Cys	His
305					310					315					320
Pro	Pro	Arg	Ser	Pro	Ala	Lys	Arg	Leu	Gln	Leu	Thr	Glu	Leu	Gln	Glu
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				405					410					415	
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			420					425					430		
Ala	Gly	Ser	Pro	Gly	Leu	Gly	Gly	Pro	Leu	Gly	Ser	Leu	Leu	Asp	Arg
		435					440					445			

